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SEQUENCE LISTING

<110> Bradfield, Christopher A.
Dolwick, Kristin M.
Carver, Lucy A.

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Detecting Agonists to the Ah Receptor

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760

765

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Asp Ser Leu Ser Lys Ser Pro Phe Ile Pro Ser Asp Tyr Gln Gln Gln	
590 595 600	
cag tcc ttg gct ctg aac tca agc tgt atg gta cag gaa cac cta cat	2236
Gln Ser Leu Ala Leu Asn Ser Ser Cys Met Val Gln Glu His Leu His	
605 610 615	
cta gaa cag caa cag caa cat cac caa aag caa gta gta gtg gag cca	2284
Leu Glu Gln Gln Gln His His Gln Lys Gln Val Val Val Glu Pro	
620 625 630	
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Gln Gln Gln Leu Cys Gln Lys Met Lys His Met Gln Val Asn Gly Met	
635 640 645 650	
ttt gaa aat tgg aac tct aac caa atc gtg cct ttc aat tgt cca cag	2380
Phe Glu Asn Trp Asn Ser Asn Gln Ile Val Pro Phe Asn Cys Pro Gln	
655 660 665	
caa gac cca caa caa tat aat gtc ttt aca gac tta cat ggg atc agt	2428
Gln Asp Pro Gln Gln Tyr Asn Val Phe Thr Asp Leu His Gly Ile Ser	
670 675 680	
caa gag ttc ccc tac aaa tct gaa atg gat tct atg cct tat aca cag	2476
Gln Glu Phe Pro Tyr Lys Ser Glu Met Asp Ser Met Pro Tyr Thr Gln	
685 690 695	
aac ttt att tcc tgt aat cag cct gta tta cca caa cat tcc aaa tgt	2524
Asn Phe Ile Ser Cys Asn Gln Pro Val Leu Pro Gln His Ser Lys Cys	
700 705 710	
aca gag ctg gac tac cct atg ggg agt ttt gaa cca tcc cca tac ccc	2572
Thr Glu Leu Asp Tyr Pro Met Gly Ser Phe Glu Pro Ser Pro Tyr Pro	
715 720 725 730	
act act tct agt tta gaa gat ttt gtc act tgt tta caa ctt cct gaa	2620
Thr Thr Ser Ser Leu Glu Asp Phe Val Thr Cys Leu Gln Leu Pro Glu	
735 740 745	
aac caa aag cat gga tta aat cca cag tca gcc ata ata act cct cag	2668
Asn Gln Lys His Gly Leu Asn Pro Gln Ser Ala Ile Ile Thr Pro Gln	
750 755 760	
aca tgt tat gct ggg gcc gtg tcg atg tat cag tgc cag cca gaa cct	2716
Thr Cys Tyr Ala Gly Ala Val Ser Met Tyr Gln Cys Gln Pro Glu Pro	
765 770 775	
cag cac acc cac gtg ggt cag atg cag tac aat cca gta ctg cca ggc	2764
Gln His Thr His Val Gly Gln Met Gln Tyr Asn Pro Val Leu Pro Gly	

780	785	790	
caa cag gca ttt tta aac aag ttt cag aat gga gtt tta aat gaa aca			2812
Gln Gln Ala Phe Leu Asn Lys Phe Gln Asn Gly Val Leu Asn Glu Thr			
795	800	805	810
tat cca gct gaa tta aat aac ata aat aac act cag act acc aca cat			2860
Tyr Pro Ala Glu Leu Asn Asn Ile Asn Asn Thr Gln Thr Thr His			
815	820	825	
ctt cag cca ctt cat cat ccg tca gaa gcc aga cct ttt cct gat ttg			2908
Leu Gln Pro Leu His His Pro Ser Glu Ala Arg Pro Phe Pro Asp Leu			
830	835	840	
aca tcc agt gga ttc ctg taa ttccaagccc aattttgacc ctgggttttg			2959
Thr Ser Ser Gly Phe Leu			
845			
gattaaatata gtttgtgaag gattatggaa aaataaaaact gtcactgttg gacgtcagca			3019
agttcacatg gaggcattga tgcatgctat tcacaattat tccaaaccaa attttaattt			3079
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ataatataatt gtgttgactt tataaatttc gcttctttaga acagtgaaaa ctatgtgtt			4099
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 20 25 30
 Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp
 35 40 45
 Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu
 50 55 60
 Asp Lys Leu Ser Val Leu Arg Leu Ser Val Ser Tyr Leu Arg Ala Lys
 65 70 75 80
 Ser Phe Phe Asp Val Ala Leu Lys Ser Ser Pro Thr Glu Arg Asn Gly
 85 90 95
 Gly Gln Asp Asn Cys Arg Ala Ala Asn Phe Arg Glu Gly Leu Asn Leu

100	105	110
Gln Glu Gly Glu Phe Leu Leu	Gln Ala Leu Asn Gly Phe Val	Leu Val
115	120	125
Val Thr Thr Asp Ala Leu Val Phe Tyr Ala Ser Ser	Thr Ile Gln Asp	
130	135	140
Tyr Leu Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val	Tyr Glu	
145	150	155
Leu Ile His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln	Leu His Trp	
165	170	175
Ala Leu Asn Pro Ser Gln Cys Thr Glu Ser Gly Gln Gly	Ile Glu Glu	
180	185	190
Ala Thr Gly Leu Pro Gln Thr Val Val Cys Tyr Asn Pro Asp	Gln Ile	
195	200	205
Pro Pro Glu Asn Ser Pro Leu Met Glu Arg Cys Phe Ile Cys Arg	Leu	
210	215	220
Arg Cys Leu Leu Asp Asn Ser Ser Gly Phe Leu Ala Met Asn	Phe Gln	
225	230	235
Gly Lys Leu Lys Tyr Leu His Gly Gln Lys Lys Lys Gly Lys	Asp Gly	
245	250	255
Ser Ile Leu Pro Pro Gln Leu Ala Leu Phe Ala Ile Ala Thr	Pro Leu	
260	265	270
Gln Pro Pro Ser Ile Leu Glu Ile Arg Thr Lys Asn Phe Ile	Phe Arg	
275	280	285
Thr Lys His Lys Leu Asp Phe Thr Pro Ile Gly Cys Asp Ala	Lys Gly	
290	295	300
Arg Ile Val Leu Gly Tyr Thr Glu Ala Glu Leu Cys Thr Arg	Gly Ser	
305	310	315
Gly Tyr Gln Phe Ile His Ala Ala Asp Met Leu Tyr Cys Ala	Glu Ser	
325	330	335
His Ile Arg Met Ile Lys Thr Gly Glu Ser Gly Met Ile Val	Phe Arg	
340	345	350
Leu Leu Thr Lys Asn Asn Arg Trp Thr Trp Val Gln Ser Asn	Ala Arg	
355	360	365
Leu Leu Tyr Lys Asn Gly Arg Pro Asp Tyr Ile Ile Val Thr	Gln Arg	
370	375	380
Pro Leu Thr Asp Glu Glu Gly Thr Glu His Leu Arg Lys Arg	Asn Thr	
385	390	395
Lys Leu Pro Phe Met Phe Thr Thr Gly Glu Ala Val Leu Tyr	Glu Ala	
405	410	415
Thr Asn Pro Phe Pro Ala Ile Met Asp Pro Leu Pro Leu	Arg Thr Lys	
420	425	430
Asn Gly Thr Ser Gly Lys Asp Ser Ala Thr Thr Ser Thr	Leu Ser Lys	
435	440	445
Asp Ser Leu Asn Pro Ser Ser Leu Leu Ala Ala Met Met	Gln Gln Asp	
450	455	460
Glu Ser Ile Tyr Leu Tyr Pro Ala Ser Ser Thr Ser Ser Thr	Ala Pro	
465	470	475
Phe Glu Asn Asn Phe Phe Asn Glu Ser Met Asn Glu Cys Arg	Asn Trp	
485	490	495
Gln Asp Asn Thr Ala Pro Met Gly Asn Asp Thr Ile Leu Lys	His Glu	
500	505	510
Gln Ile Asp Gln Pro Gln Asp Val Asn Ser Phe Ala Gly	Gly His Pro	
515	520	525
Gly Leu Phe Gln Asp Ser Lys Asn Ser Asp Leu Tyr Ser Ile	Met Lys	
530	535	540
Asn Leu Gly Ile Asp Phe Glu Asp Ile Arg His Met Gln Asn	Glu Lys	
545	550	555
Phe Phe Arg Asn Asp Phe Ser Gly Glu Val Asp Phe Arg Asp	Ile Asp	

565	570	575	
Leu Thr Asp Glu Ile Leu Thr Tyr Val Gln Asp Ser Leu Ser Lys Ser			
580	585	590	
Pro Phe Ile Pro Ser Asp Tyr Gln Gln Gln Ser Leu Ala Leu Asn			
595	600	605	
Ser Ser Cys Met Val Gln Glu His Leu His Leu Glu Gln Gln Gln			
610	615	620	
His His Gln Lys Gln Val Val Val Glu Pro Gln Gln Gln Leu Cys Gln			
625	630	635	640
Lys Met Lys His Met Gln Val Asn Gly Met Phe Glu Asn Trp Asn Ser			
645	650	655	
Asn Gln Ile Val Pro Phe Asn Cys Pro Gln Gln Asp Pro Gln Gln Tyr			
660	665	670	
Asn Val Phe Thr Asp Leu His Gly Ile Ser Gln Glu Phe Pro Tyr Lys			
675	680	685	
Ser Glu Met Asp Ser Met Pro Tyr Thr Gln Asn Phe Ile Ser Cys Asn			
690	695	700	
Gln Pro Val Leu Pro Gln His Ser Lys Cys Thr Glu Leu Asp Tyr Pro			
705	710	715	720
Met Gly Ser Phe Glu Pro Ser Pro Tyr Pro Thr Thr Ser Ser Leu Glu			
725	730	735	
Asp Phe Val Thr Cys Leu Gln Leu Pro Glu Asn Gln Lys His Gly Leu			
740	745	750	
Asn Pro Gln Ser Ala Ile Ile Thr Pro Gln Thr Cys Tyr Ala Gly Ala			
755	760	765	
Val Ser Met Tyr Gln Cys Gln Pro Glu Pro Gln His Thr His Val Gly			
770	775	780	
Gln Met Gln Tyr Asn Pro Val Leu Pro Gly Gln Gln Ala Phe Leu Asn			
785	790	795	800
Lys Phe Gln Asn Gly Val Leu Asn Glu Thr Tyr Pro Ala Glu Leu Asn			
805	810	815	
Asn Ile Asn Asn Thr Gln Thr Thr His Leu Gln Pro Leu His His			
820	825	830	
Pro Ser Glu Ala Arg Pro Phe Pro Asp Leu Thr Ser Ser Gly Phe Leu			
835	840	845	

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<211> 52
<212> DNA
<213> murine

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<222> (3)
<223> i

<220>
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<220>
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<400> 5
ttnatncctc tcngcnggna tnggtcttna cngttctttc tgnacnggtc tt      52

<210> 6
<211> 20
<212> DNA
<213> murine

<220>
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<222> (7)
<223> Can be either adenine, thymine, guanosine or
      cytosine.

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<222> (10)
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      cytosine.

<400> 6
aaagccngtn caagaaagac

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<210> 7		
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gaagatcttc cagtggtccc agcctacacc		30
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gctctagatg atcaccatgg tgcagaagac cgtgaagccc atccccgtg aaggaattaa	60	
gtc	63	
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<211> 63		

<212> DNA
<213> murine

<400> 13
gcactagttg atcaccatgg ccagccgcaa gcggcgcaag ccgggtgcaga agaccgtgaa 60
gcc 63

<210> 14
<211> 65
<212> DNA
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<400> 14
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caagc 65

<210> 15
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<212> DNA
<213> murine

<400> 15
gcagagtctg ggtagagc 20

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic sequence

<400> 16
tcgagtagat cacgcaatgg gcccagc 27

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic sequence

<400> 17
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<210> 18
<211> 28
<212> DNA
<213> Unknown Organism

<220>
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<400> 18
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<210> 19
<211> 40
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

<400> 19
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<210> 20
<211> 36
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

<400> 20
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<210> 21
<211> 36
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

<400> 21
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<210> 22
<211> 49
<212> DNA
<213> Unknown Organism

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<210> 23
<211> 37
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<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

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<212> DNA
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<223> Description of Unknown Organism: Unknown

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<210> 25
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<210> 27
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<400> 27
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<210> 28

<211> 34
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<210> 30
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<210> 31
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<220>
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<210> 32
<211> 38
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Unknown

<400> 32
ataagaatgc ggccgcagcc ccccccgaccg atgtcagc 38

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<210> 33
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<211> 36
<212> DNA
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<220>
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<210> 36
<211> 40
<212> DNA
<213> Unknown Organism

<220>
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<210> 37
<211> 72
<212> PRT
<213> human

<400> 37
Arg Lys Arg Arg Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala
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Glu Gly Ile Lys Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn

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20

25

30

Thr Glu Leu Asp Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val
 35 40 45

Ile Asn Lys Leu Asp Lys Leu Ser Val Leu Arg Leu Ser Val Ser Tyr
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Leu Arg Ala Lys Ser Phe Phe Asp
 65 70

<210> 38

<211> 72

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: unknown

<400> 38

Arg Lys Arg Arg Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala
 1 5 10 15

Glu Gly Ile Lys Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn
 20 25 30

Thr Glu Leu Asp Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val
 35 40 45

Ile Asn Lys Leu Asp Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr
 50 55 60

Leu Arg Ala Lys Ser Phe Phe Asp
 65 70

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<211> 208

<212> PRT

<213> human

<400> 39

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Glu Ser Gly Gln Gly Ile Glu Glu Ala Thr Gly Leu Pro Gln Thr Val
 20 25 30

Val Cys Tyr Asn Pro Asp Gln Ile Pro Pro Glu Asn Ser Pro Leu Met
 35 40 45

Glu Arg Cys Phe Ile Cys Arg Leu Arg Cys Leu Leu Asp Asn Ser Ser
 50 55 60

Gly Phe Leu Ala Met Asn Phe Gln Gly Lys Leu Lys Tyr Leu His Gly
 65 70 75 80

Gln Lys Lys Lys Gly Lys Asp Gly Ser Ile Leu Pro Pro Gln Leu Ala
 85 90 95
 Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu Glu Ile
 100 105 110
 Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp Phe Thr
 115 120 125
 Pro Ile Gly Cys Asp Ala Lys Gly Arg Ile Val Leu Gly Tyr Thr Glu
 130 135 140
 Ala Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His Ala Ala
 145 150 155 160
 Asp Met Leu Tyr Cys Ala Glu Ser His Ile Arg Met Ile Lys Thr Gly
 165 170 175
 Glu Ser Gly Met Ile Val Phe Arg Leu Leu Thr Lys Asn Asn Arg Trp
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 Thr Trp Val Gln Ser Asn Ala Arg Leu Leu Tyr Lys Asn Gly Arg Pro
 195 200 205

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 <212> PRT
 <213> murine

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 Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser Phe Met Glu Arg Cys Phe
 35 40 45
 Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn Ser Ser Gly Phe Leu Ala
 50 55 60
 Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu His Gly Gln Asn Lys Lys
 65 70 75 80
 Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln Leu Ala Leu Phe Ala Ile
 85 90 95
 Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu Glu Ile Arg Thr Lys Asn
 100 105 110
 Phe Ile Phe Arg Thr Lys His Lys Leu Asp Phe Thr Pro Ile Gly Cys
 115 120 125

Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr Thr Glu Val Glu Leu Cys
130 135 140

Thr Arg Gly Ser Gly Tyr Gln Phe Ile His Ala Ala Asp Ile Leu His
145 150 155 160

Cys Ala Glu Ser His Ile Arg Met Ile Lys Thr Gly Glu Ser Gly Met
165 170 175

Thr Val Phe Arg Leu Leu Ala Lys His Ser Arg Trp Arg Trp Val Gln
180 185 190

Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly Arg Pro
195 200